



SEQUENCE LISTING

<110> MIYATA, Toshio

<120> A Method for Detecting Megsin Protein and Use
Thereof

<130> SHIM-012

<140> 09/936,883

<141> 2001-12-21

<150> JP 1999-75305

<151> 1999-03-19

<150> JP 1999-306623

<151> 1999-10-28

<160> 21

<170> PatentIn Ver. 2.0

<210> 1

<211> 1143

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1140)

<300>

<302> A mesangium-predominant gene, megsin, is a new serpin
upregulated in IgA nephropathy.

<303> J. Clin. Invest.

<304> 120

<305> 4

<306> 828-836

<307> 1998-08-15

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1 5 10 15	
aga gag atg gat gac aat caa gga aat gga aat gtg ttc ttt tcc tct	96
Arg Glu Met Asp Asp Asn Gln Gly Asn Gly Asn Val Phe Phe Ser Ser	
20 25 30	
ctg agc ctc ttc gct gcc ctg gcc ctg gtc cgc ttg ggc gct caa gat	144
Leu Ser Leu Phe Ala Ala Leu Ala Leu Val Arg Leu Gly Ala Gln Asp	
35 40 45	
gac tcc ctc tct cag att gat aag ttg ctt cat gtt aac act gcc tca	192
Asp Ser Leu Ser Gln Ile Asp Lys Leu Leu His Val Asn Thr Ala Ser	
50 55 60	

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gga tat gga aac tct tct aat agt cag tca ggg ctc cag tct caa ctg	240
Gly Tyr Gly Asn Ser Ser Asn Ser Gln Ser Gly Leu Gln Ser Gln Leu	
65 70 75 80	
aaa aga gtt ttt tct gat ata aat gca tcc cac aag gat tat gat ctc	288
Lys Arg Val Phe Ser Asp Ile Asn Ala Ser His Lys Asp Tyr Asp Leu	
85 90 95	
agc att gtg aat ggg ctt ttt gct gaa aaa gtg tat ggc ttt cat aag	336
Ser Ile Val Asn Gly Leu Phe Ala Glu Lys Val Tyr Gly Phe His Lys	
100 105 110	
gac tac att gag tgt gcc gaa aaa tta tac gat gcc aaa gtg gag cga	384
Asp Tyr Ile Glu Cys Ala Glu Lys Leu Tyr Asp Ala Lys Val Glu Arg	
115 120 125	
gtt gac ttt acg aat cat tta gaa gac act aga cgt aat att aat aag	432
Val Asp Phe Thr Asn His Leu Glu Asp Thr Arg Arg Asn Ile Asn Lys	
130 135 140	
tgg gtt gaa aat gaa aca cat ggc aaa atc aag aac gtg att ggt gaa	480
Trp Val Glu Asn Glu Thr His Gly Lys Ile Lys Asn Val Ile Gly Glu	
145 150 155 160	
ggt ggc ata agc tca tct gct gta atg gtg ctg gtg aat gct gtg tac	528
Gly Gly Ile Ser Ser Ser Ala Val Met Val Leu Val Asn Ala Val Tyr	
165 170 175	
ttc aaa ggc aag tgg caa tca gcc ttc acc aag agc gaa acc ata aat	576
Phe Lys Gly Lys Trp Gln Ser Ala Phe Thr Lys Ser Glu Thr Ile Asn	
180 185 190	
tgc cat ttc aaa tct ccc aag tgc tct ggg aag gca gtc gcc atg atg	624
Cys His Phe Lys Ser Pro Lys Cys Ser Gly Lys Ala Val Ala Met Met	
195 200 205	
cat cag gaa cgg aag ttc aat ttg tct gtt att gag gac cca tca atg	672
His Gln Glu Arg Lys Phe Asn Leu Ser Val Ile Glu Asp Pro Ser Met	
210 215 220	
aag att ctt gag ctc aga tac aat ggt ggc ata aac atg tac gtt ctg	720
Lys Ile Leu Glu Leu Arg Tyr Asn Gly Gly Ile Asn Met Tyr Val Leu	
225 230 235 240	
ctg cct gag aat gac ctc tct gaa att gaa aac aaa ctg acc ttt cag	768
Leu Pro Glu Asn Asp Leu Ser Glu Ile Glu Asn Lys Leu Thr Phe Gln	
245 250 255	
aat cta atg gaa tgg acc aat cca agg cga atg acc tct aag tat gtt	816
Asn Leu Met Glu Trp Thr Asn Pro Arg Arg Met Thr Ser Lys Tyr Val	
260 265 270	
gag gta ttt ttt cct cag ttc aag ata gag aag aat tat gaa atg aaa	864
Glu Val Phe Phe Pro Gln Phe Lys Ile Glu Lys Asn Tyr Glu Met Lys	
275 280 285	
caa tat ttg aga gcc cta ggg ctg aaa gat atc ttt gat gaa tcc aaa	912

Gln	Tyr	Leu	Arg	Ala	Leu	Gly	Leu	Lys	Asp	Ile	Phe	Asp	Glu	Ser	Lys	
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gca	gat	ctc	tct	ggg	att	gct	tcg	ggg	ggt	cgt	ctg	tat	ata	tca	agg	960
Ala	Asp	Leu	Ser	Gly	Ile	Ala	Ser	Gly	Gly	Arg	Leu	Tyr	Ile	Ser	Arg	
305				310					315					320		
atg	atg	cac	aaa	tct	tac	ata	gag	gtc	act	gag	gag	ggc	acc	gag	gct	1008
Met	Met	His	Lys	Ser	Tyr	Ile	Glu	Val	Thr	Glu	Glu	Gly	Thr	Glu	Ala	
			325					330					335			
act	gct	gcc	aca	gga	agt	aat	att	gta	gaa	aag	caa	ctc	cct	cag	tcc	1056
Thr	Ala	Ala	Thr	Gly	Ser	Asn	Ile	Val	Glu	Lys	Gln	Leu	Pro	Gln	Ser	
			340					345					350			
acg	ctg	ttt	aga	gct	gac	cac	cca	ttc	cta	ttt	gtt	atc	agg	aag	gat	1104
Thr	Leu	Phe	Arg	Ala	Asp	His	Pro	Phe	Leu	Phe	Val	Ile	Arg	Lys	Asp	
		355					360					365				
gac	atc	atc	tta	ttc	agt	ggc	aaa	gtt	tct	tgc	cct	tga				1143
Asp	Ile	Ile	Leu	Phe	Ser	Gly	Lys	Val	Ser	Cys	Pro					
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 <212> PRT
 <213> Homo sapiens

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Leu	Ser	Leu	Phe	Ala	Ala	Leu	Ala	Leu	Val	Arg	Leu	Gly	Ala	Gln	Asp	
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Asp	Ser	Leu	Ser	Gln	Ile	Asp	Lys	Leu	Leu	His	Val	Asn	Thr	Ala	Ser	
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Gly	Tyr	Gly	Asn	Ser	Ser	Asn	Ser	Gln	Ser	Gly	Leu	Gln	Ser	Gln	Leu	
	65				70					75					80	
Lys	Arg	Val	Phe	Ser	Asp	Ile	Asn	Ala	Ser	His	Lys	Asp	Tyr	Asp	Leu	
				85				90						95		
Ser	Ile	Val	Asn	Gly	Leu	Phe	Ala	Glu	Lys	Val	Tyr	Gly	Phe	His	Lys	
			100					105					110			
Asp	Tyr	Ile	Glu	Cys	Ala	Glu	Lys	Leu	Tyr	Asp	Ala	Lys	Val	Glu	Arg	
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Val	Asp	Phe	Thr	Asn	His	Leu	Glu	Asp	Thr	Arg	Arg	Asn	Ile	Asn	Lys	
	130					135						140				

Trp	Val	Glu	Asn	Glu	Thr	His	Gly	Lys	Ile	Lys	Asn	Val	Ile	Gly	Glu	145	150	155	160
Gly	Gly	Ile	Ser	Ser	Ser	Ala	Val	Met	Val	Leu	Val	Asn	Ala	Val	Tyr	165	170	175	
Phe	Lys	Gly	Lys	Trp	Gln	Ser	Ala	Phe	Thr	Lys	Ser	Glu	Thr	Ile	Asn	180	185	190	
Cys	His	Phe	Lys	Ser	Pro	Lys	Cys	Ser	Gly	Lys	Ala	Val	Ala	Met	Met	195	200	205	
His	Gln	Glu	Arg	Lys	Phe	Asn	Leu	Ser	Val	Ile	Glu	Asp	Pro	Ser	Met	210	215	220	
Lys	Ile	Leu	Glu	Leu	Arg	Tyr	Asn	Gly	Gly	Ile	Asn	Met	Tyr	Val	Leu	225	230	235	240
Leu	Pro	Glu	Asn	Asp	Leu	Ser	Glu	Ile	Glu	Asn	Lys	Leu	Thr	Phe	Gln	245	250	255	
Asn	Leu	Met	Glu	Trp	Thr	Asn	Pro	Arg	Arg	Met	Thr	Ser	Lys	Tyr	Val	260	265	270	
Glu	Val	Phe	Phe	Pro	Gln	Phe	Lys	Ile	Glu	Lys	Asn	Tyr	Glu	Met	Lys	275	280	285	
Gln	Tyr	Leu	Arg	Ala	Leu	Gly	Leu	Lys	Asp	Ile	Phe	Asp	Glu	Ser	Lys	290	295	300	
Ala	Asp	Leu	Ser	Gly	Ile	Ala	Ser	Gly	Gly	Arg	Leu	Tyr	Ile	Ser	Arg	305	310	315	320
Met	Met	His	Lys	Ser	Tyr	Ile	Glu	Val	Thr	Glu	Glu	Gly	Thr	Glu	Ala	325	330	335	
Thr	Ala	Ala	Thr	Gly	Ser	Asn	Ile	Val	Glu	Lys	Gln	Leu	Pro	Gln	Ser	340	345	350	
Thr	Leu	Phe	Arg	Ala	Asp	His	Pro	Phe	Leu	Phe	Val	Ile	Arg	Lys	Asp	355	360	365	
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<211> 29

<212> DNA

<213> Artificial Sequence

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<400> 3
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29

<210> 4
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<220>
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synthesized degenerative primer sequence

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<400> 4
aanagraang grtcngc

17

<210> 5
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<212> DNA
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<220>
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<220>
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<223> n is a or g or c or t.

<400> 5
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<210> 6
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
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synthesized degenerative primer sequence

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<210> 7

<211> 34
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<210> 8
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 <212> DNA
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<210> 9
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 <212> DNA
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<210> 10
 <211> 36
 <212> DNA
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence:Artificially
 synthesized sense primer sequence

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<210> 11
 <211> 15
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<223> Description of Artificial Sequence:Artificially
synthesized domain peptide of human megsin

<400> 11

Phe Arg Glu Met Asp Asp Asn Gln Gly Asn Gly Asn Val Phe Phe
1 5 10 15

<210> 12

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
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<400> 12

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1 5 10 15

<210> 13

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
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Ala Thr Gly Ser Asn Ile Val Glu Lys Gln Leu Pro Gln Ser Thr Leu
1 5 10 15

<210> 14

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially
synthesized domain peptide of human megsin

<400> 14

Asn Leu Met Glu Trp Thr Asn Pro Arg Arg Met Thr Ser Lys Tyr Val
1 5 10 15

<210> 15

<211> 15

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
synthesized domain peptide of human megsin

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 1 5 10 15

<210> 16
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<220>
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 synthesized domain peptide of human megsin

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<210> 17
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<210> 18
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 <212> DNA
 <213> Rattus norvegicus

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 <222> (8)..(1147)

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 <310> PCT/JP98/04269
 <311> 1998-09-22

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Leu	Phe	Arg	Glu	Met	Asp	Ser	Ser	Gln	Gly	Asn	Gly	Asn	Val	Phe	Phe	
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tct	tcc	ctg	agc	atc	ttc	act	gcc	ctg	agc	cta	atc	cgt	ttg	ggg	gct	145
Ser	Ser	Leu	Ser	Ile	Phe	Thr	Ala	Leu	Ser	Leu	Ile	Arg	Leu	Gly	Ala	
				35					40					45		
cga	ggg	gac	tgt	nnn	cgt	cag	att	gac	aag	gcc	ctg	cac	ttt	atc	tcc	193
Arg	Gly	Asp	Cys	Xaa	Arg	Gln	Ile	Asp	Lys	Ala	Leu	His	Phe	Ile	Ser	
			50					55					60			
cca	tca	aga	caa	ggg	aat	tca	tcg	aac	agt	cag	cta	gga	ctg	caa	tat	241
Pro	Ser	Arg	Gln	Gly	Asn	Ser	Ser	Asn	Ser	Gln	Leu	Gly	Leu	Gln	Tyr	
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caa	ttg	aaa	aga	gtt	ctt	gct	gac	ata	aac	tca	tct	cat	aag	gat	nnn	289
Gln	Leu	Lys	Arg	Val	Leu	Ala	Asp	Ile	Asn	Ser	Ser	His	Lys	Asp	Xaa	
	80					85					90					
aaa	ctc	agc	att	gcc	aat	gga	gtt	ttt	gca	gag	aaa	gta	ttt	gat	ttt	337
Lys	Leu	Ser	Ile	Ala	Asn	Gly	Val	Phe	Ala	Glu	Lys	Val	Phe	Asp	Phe	
	95				100					105					110	
cat	aag	agc	tat	atg	gag	tgt	gct	gaa	aac	tta	tac	aat	gct	aaa	gtg	385
His	Lys	Ser	Tyr	Met	Glu	Cys	Ala	Glu	Asn	Leu	Tyr	Asn	Ala	Lys	Val	
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gaa	aga	gtt	gat	ttt	aca	aat	gat	ata	caa	gaa	acc	aga	ttt	aaa	att	433
Glu	Arg	Val	Asp	Phe	Thr	Asn	Asp	Ile	Gln	Glu	Thr	Arg	Phe	Lys	Ile	
			130					135					140			
aat	aaa	tgg	att	gaa	aat	gaa	aca	cat	ggc	aaa	atc	aag	aag	gtg	ttg	481
Asn	Lys	Trp	Ile	Glu	Asn	Glu	Thr	His	Gly	Lys	Ile	Lys	Lys	Val	Leu	
		145					150					155				
ggg	gac	agc	agc	ctc	agc	tca	tca	gct	gtc	atg	gtg	cta	gtg	aat	gct	529
Gly	Asp	Ser	Ser	Leu	Ser	Ser	Ser	Ala	Val	Met	Val	Leu	Val	Asn	Ala	
	160					165					170					
gtt	tac	ttc	aaa	ggc	aag	tgg	aaa	tcg	gcc	ttc	acc	aag	agt	gat	acc	577
Val	Tyr	Phe	Lys	Gly	Lys	Trp	Lys	Ser	Ala	Phe	Thr	Lys	Ser	Asp	Thr	
	175				180					185					190	
ctc	agt	tgc	cat	ttc	agg	tct	ccc	agc	ggg	cct	gga	aaa	gca	gtt	aat	625
Leu	Ser	Cys	His	Phe	Arg	Ser	Pro	Ser	Gly	Pro	Gly	Lys	Ala	Val	Asn	
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atg	atg	cat	caa	gaa	cgg	agg	ttc	aat	ttg	tct	acc	att	cag	gag	cca	673
Met	Met	His	Gln	Glu	Arg	Arg	Phe	Asn	Leu	Ser	Thr	Ile	Gln	Glu	Pro	
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cca	atg	cag	att	ctt	gag	cta	caa	tat	cat	ggg	ggc	ata	agc	atg	tac	721
Pro	Met	Gln	Ile	Leu	Glu	Leu	Gln	Tyr	His	Gly	Gly	Ile	Ser	Met	Tyr	
		225					230					235				
atc	atg	ttg	ccc	gag	gat	gac	cta	tcc	gaa	att	gaa	agc	aag	ctg	agt	769
Ile	Met	Leu	Pro	Glu	Asp	Asp	Leu	Ser	Glu	Ile	Glu	Ser	Lys	Leu	Ser	

240	245	250	
ttc cag aat cta atg gac tgg aca aat agc agg aag atg aaa tct cag			817
Phe Gln Asn Leu Met Asp Trp Thr Asn Ser Arg Lys Met Lys Ser Gln			
255	260	265	270
tat gtg aat gtg ttt ctc ccc cag ttc aag ata gag aaa gat tat gaa			865
Tyr Val Asn Val Phe Leu Pro Gln Phe Lys Ile Glu Lys Asp Tyr Glu			
	275	280	285
atg agg agc cac ttg aaa tct gta ggc ttg gaa gac atc ttt gtt gag			913
Met Arg Ser His Leu Lys Ser Val Gly Leu Glu Asp Ile Phe Val Glu			
	290	295	300
tcc agg gct gat ctg tct gga att gcc tct gga ggt cgt ctc tat gta			961
Ser Arg Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Val			
	305	310	315
tca aag cta atg cac aag tcc ctc ata gag gtc tca gaa gaa ggc acc			1009
Ser Lys Leu Met His Lys Ser Leu Ile Glu Val Ser Glu Glu Gly Thr			
	320	325	330
gag gca act gct gcc aca gaa agt aac atc gtt gaa aag cta ctt cct			1057
Glu Ala Thr Ala Ala Thr Glu Ser Asn Ile Val Glu Lys Leu Leu Pro			
	335	340	345
gaa tcc acg gtg ttc aga gct gac cgc ccc ttt ctg ttt gtc att agg			1105
Glu Ser Thr Val Phe Arg Ala Asp Arg Pro Phe Leu Phe Val Ile Arg			
	355	360	365
aag aat ggc atc atc tta ttt act ggc aaa gtc tcg tgt cct			1147
Lys Asn Gly Ile Ile Leu Phe Thr Gly Lys Val Ser Cys Pro			
	370	375	380
tgaaattcta ttgtgttttc catacactaa caggcatgaa gaaacatcat aagtgaatag			1207
aattgtaatt ggaagtacat gg			1229

<210> 19
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 <212> PRT
 <213> Rattus norvegicus

<220>
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 <222> 51, 94
 <223> Xaa is unknown.

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 Leu Ser Ile Phe Thr Ala Leu Ser Leu Ile Arg Leu Gly Ala Arg Gly

35	40	45																	
Asp	Cys	Xaa	Arg	Gln	Ile	Asp	Lys	Ala	Leu	His	Phe	Ile	Ser	Pro	Ser				
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Arg	Gln	Gly	Asn	Ser	Ser	Asn	Ser	Gln	Leu	Gly	Leu	Gln	Tyr	Gln	Leu				
65					70					75					80				
Lys	Arg	Val	Leu	Ala	Asp	Ile	Asn	Ser	Ser	His	Lys	Asp	Xaa	Lys	Leu				
				85					90					95					
Ser	Ile	Ala	Asn	Gly	Val	Phe	Ala	Glu	Lys	Val	Phe	Asp	Phe	His	Lys				
			100					105					110						
Ser	Tyr	Met	Glu	Cys	Ala	Glu	Asn	Leu	Tyr	Asn	Ala	Lys	Val	Glu	Arg				
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Val	Asp	Phe	Thr	Asn	Asp	Ile	Gln	Glu	Thr	Arg	Phe	Lys	Ile	Asn	Lys				
	130					135					140								
Trp	Ile	Glu	Asn	Glu	Thr	His	Gly	Lys	Ile	Lys	Lys	Val	Leu	Gly	Asp				
145					150					155					160				
Ser	Ser	Leu	Ser	Ser	Ser	Ala	Val	Met	Val	Leu	Val	Asn	Ala	Val	Tyr				
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Phe	Lys	Gly	Lys	Trp	Lys	Ser	Ala	Phe	Thr	Lys	Ser	Asp	Thr	Leu	Ser				
			180					185					190						
Cys	His	Phe	Arg	Ser	Pro	Ser	Gly	Pro	Gly	Lys	Ala	Val	Asn	Met	Met				
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His	Gln	Glu	Arg	Arg	Phe	Asn	Leu	Ser	Thr	Ile	Gln	Glu	Pro	Pro	Met				
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Gln	Ile	Leu	Glu	Leu	Gln	Tyr	His	Gly	Gly	Ile	Ser	Met	Tyr	Ile	Met				
225					230					235					240				
Leu	Pro	Glu	Asp	Asp	Leu	Ser	Glu	Ile	Glu	Ser	Lys	Leu	Ser	Phe	Gln				
			245						250					255					
Asn	Leu	Met	Asp	Trp	Thr	Asn	Ser	Arg	Lys	Met	Lys	Ser	Gln	Tyr	Val				
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Asn	Val	Phe	Leu	Pro	Gln	Phe	Lys	Ile	Glu	Lys	Asp	Tyr	Glu	Met	Arg				
	275						280					285							
Ser	His	Leu	Lys	Ser	Val	Gly	Leu	Glu	Asp	Ile	Phe	Val	Glu	Ser	Arg				
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Ala	Asp	Leu	Ser	Gly	Ile	Ala	Ser	Gly	Gly	Arg	Leu	Tyr	Val	Ser	Lys				
305					310					315					320				
Leu	Met	His	Lys	Ser	Leu	Ile	Glu	Val	Ser	Glu	Glu	Gly	Thr	Glu	Ala				
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Thr	Ala	Ala	Thr	Glu	Ser	Asn	Ile	Val	Glu	Lys	Leu	Leu	Pro	Glu	Ser				

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Gly Ile Ile Leu Phe Thr Gly Lys Val Ser Cys Pro
 370 375 380

<210> 20
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 <213> Mus musculus

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 <222> (1)..(1104)

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 <311> 1998-09-22

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